

330/345

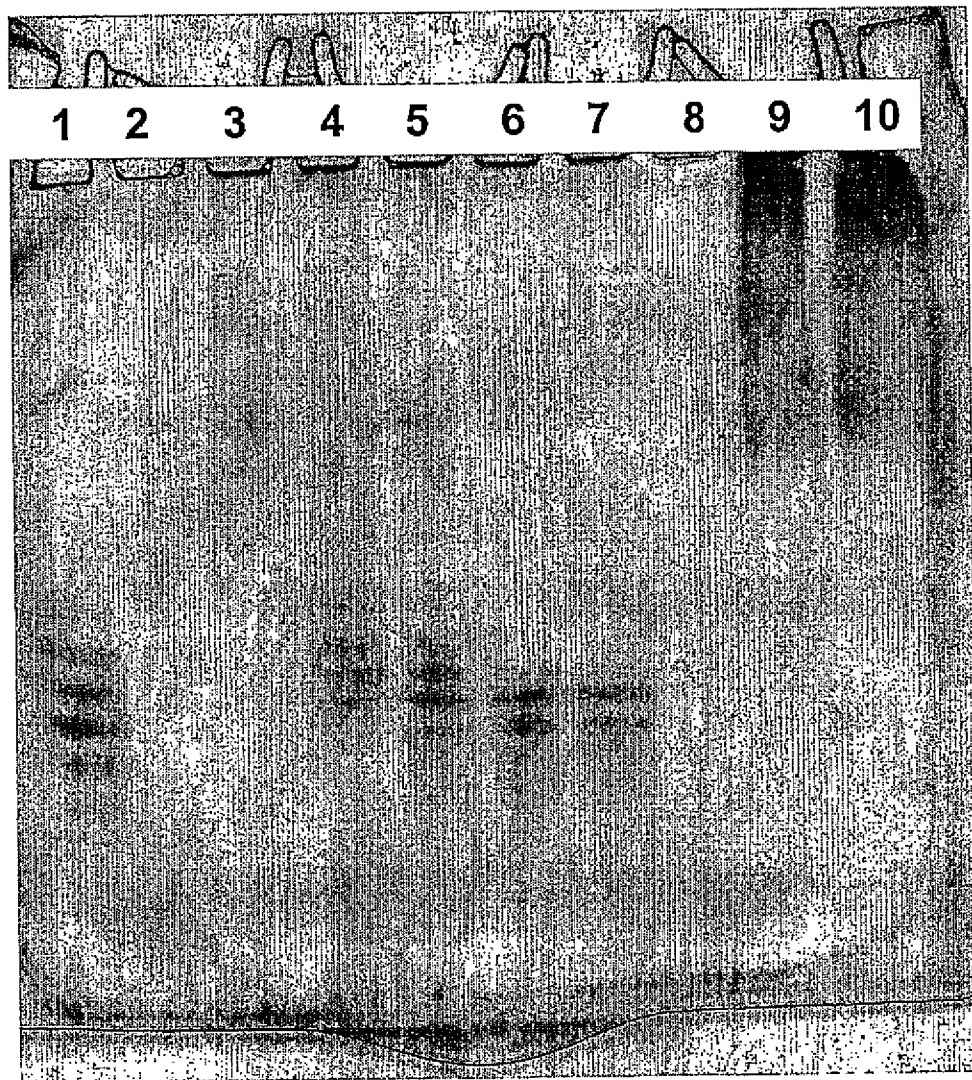


FIG. 111

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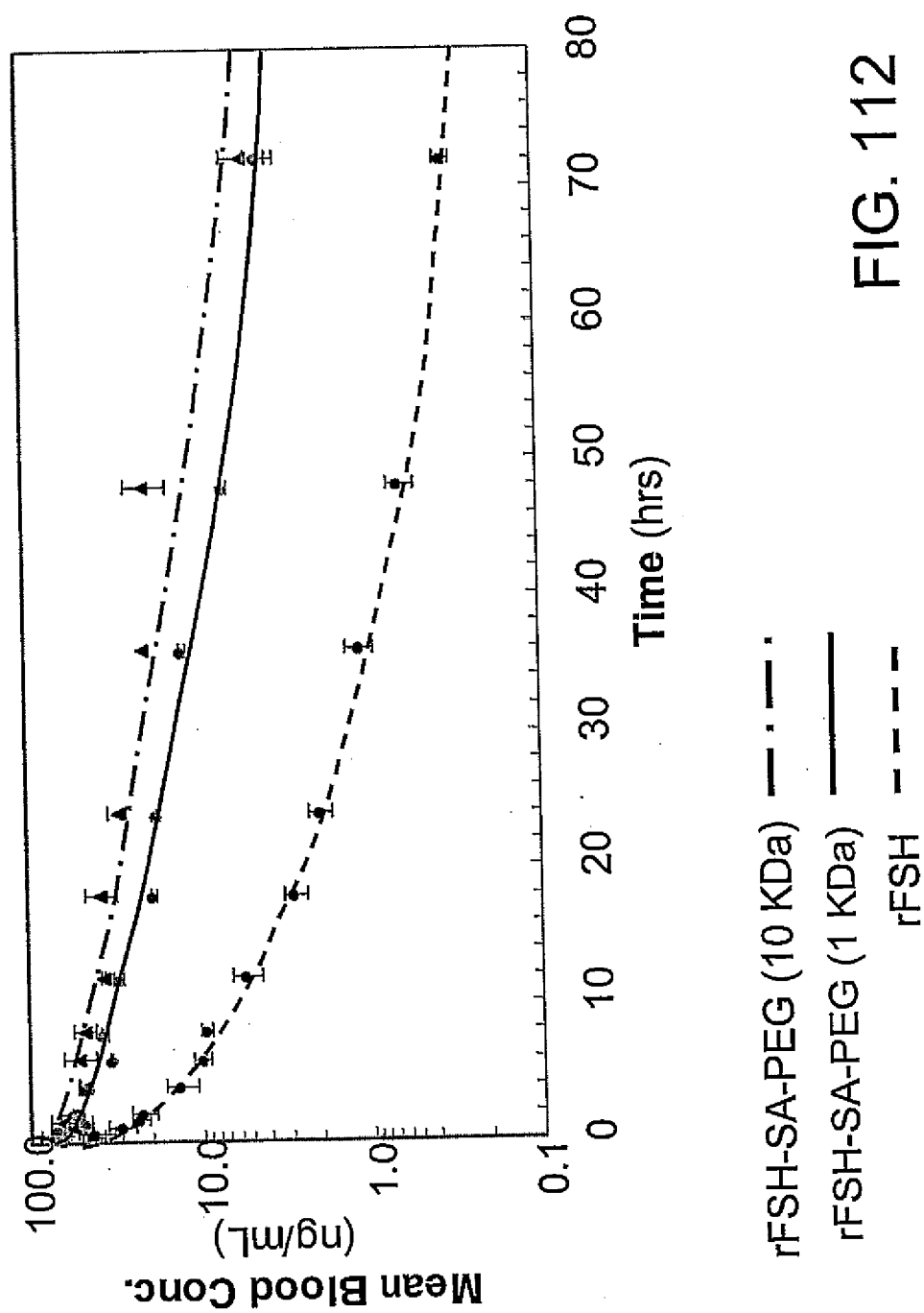


FIG. 112

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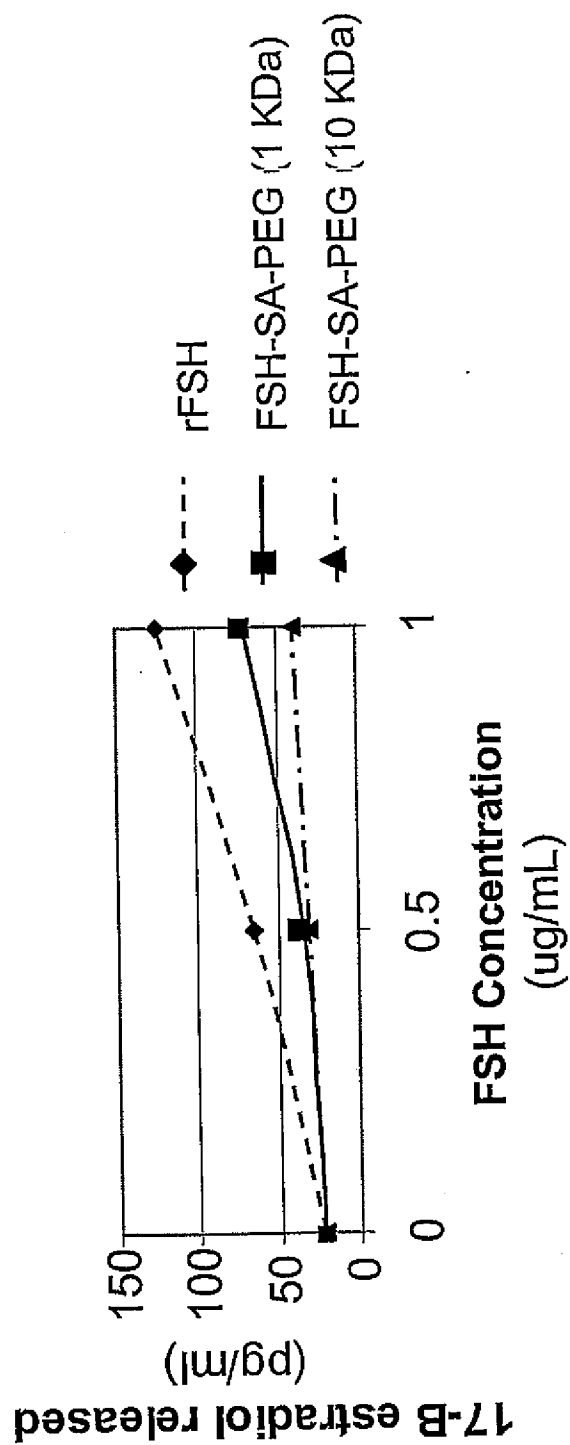


FIG. 113

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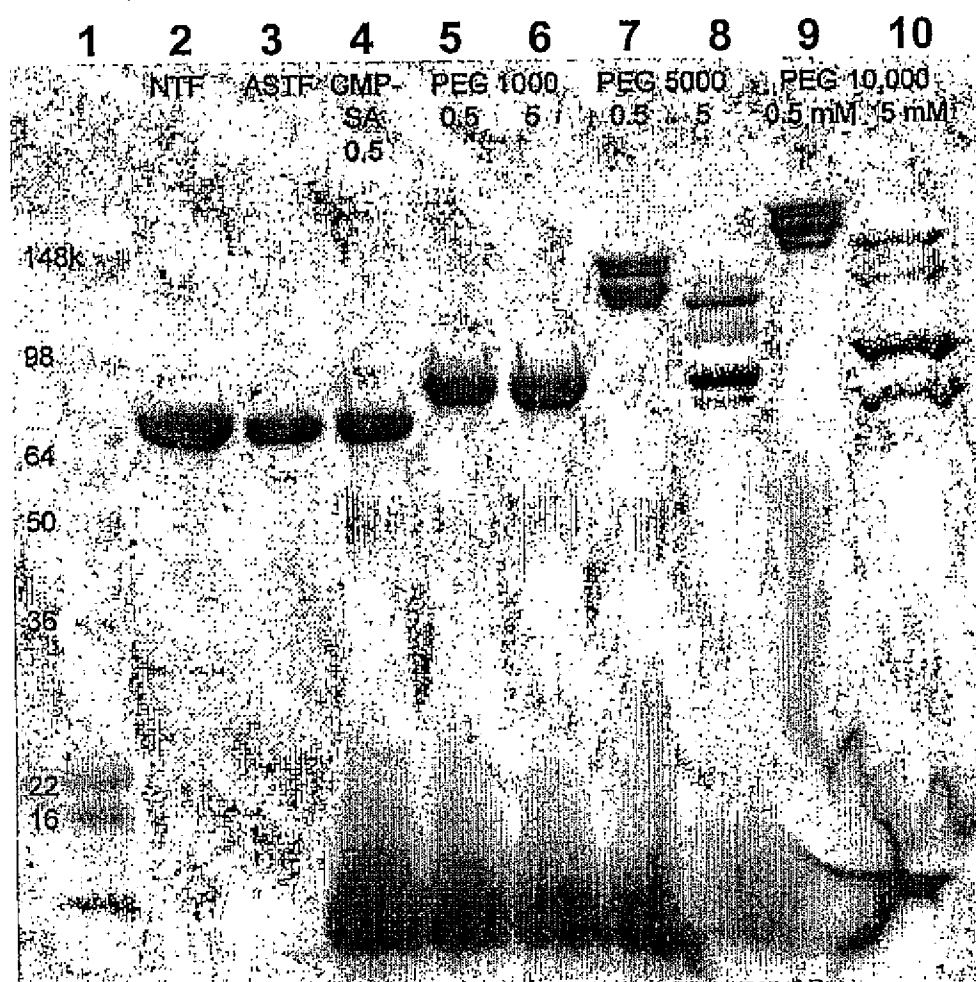


FIG. 114

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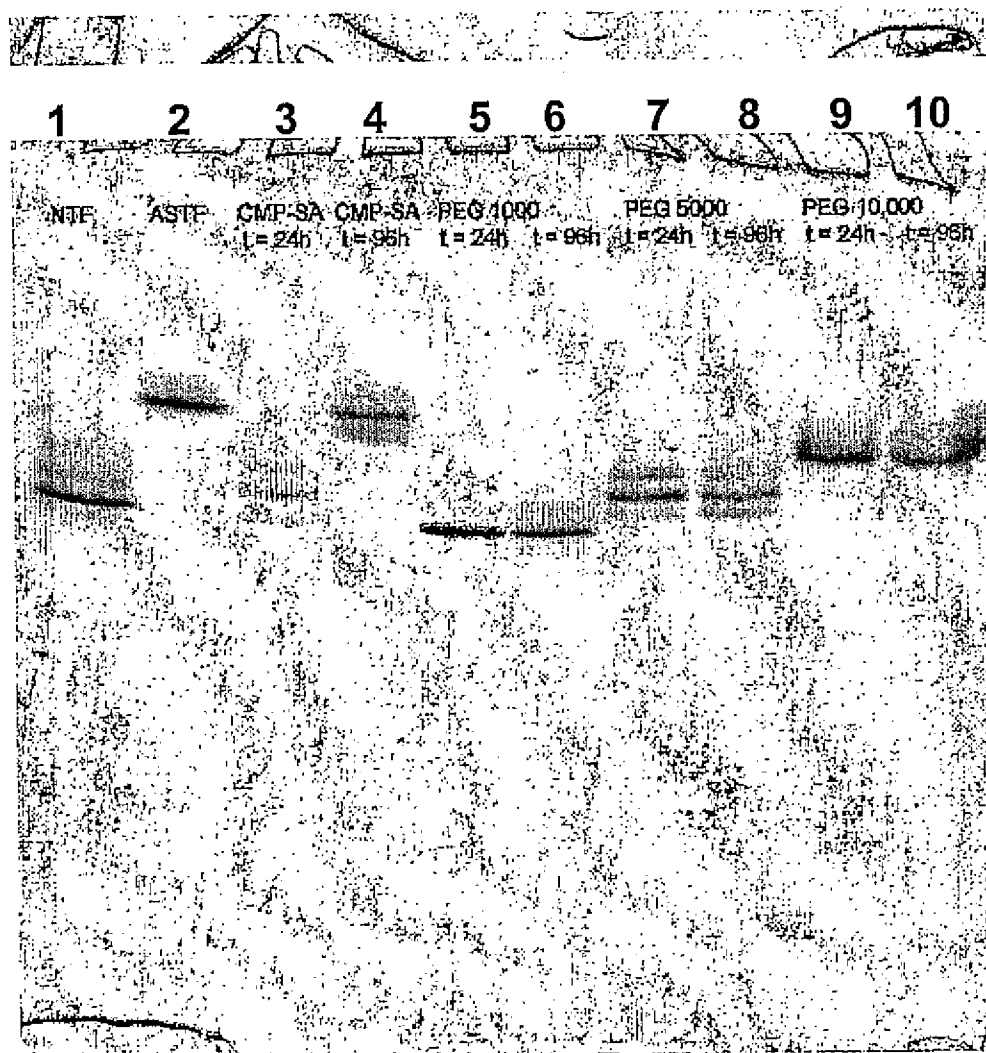


FIG. 115

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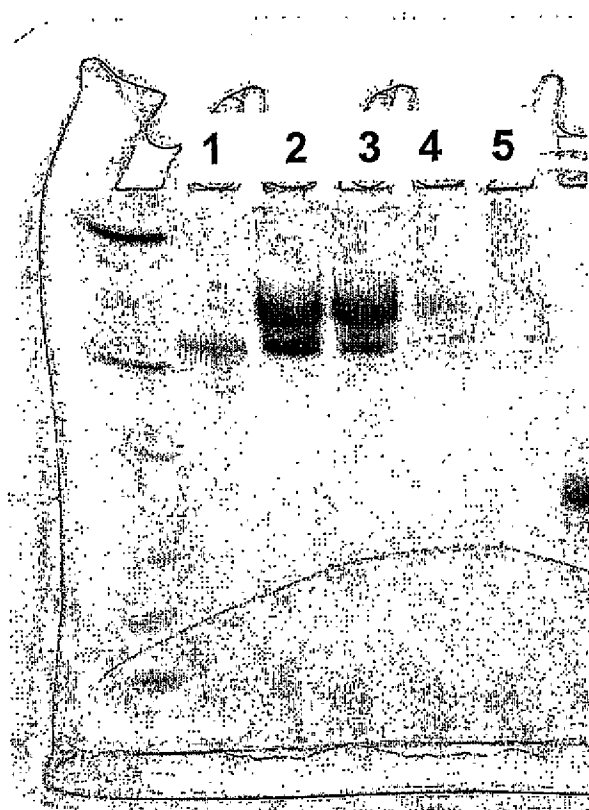


FIG. 116

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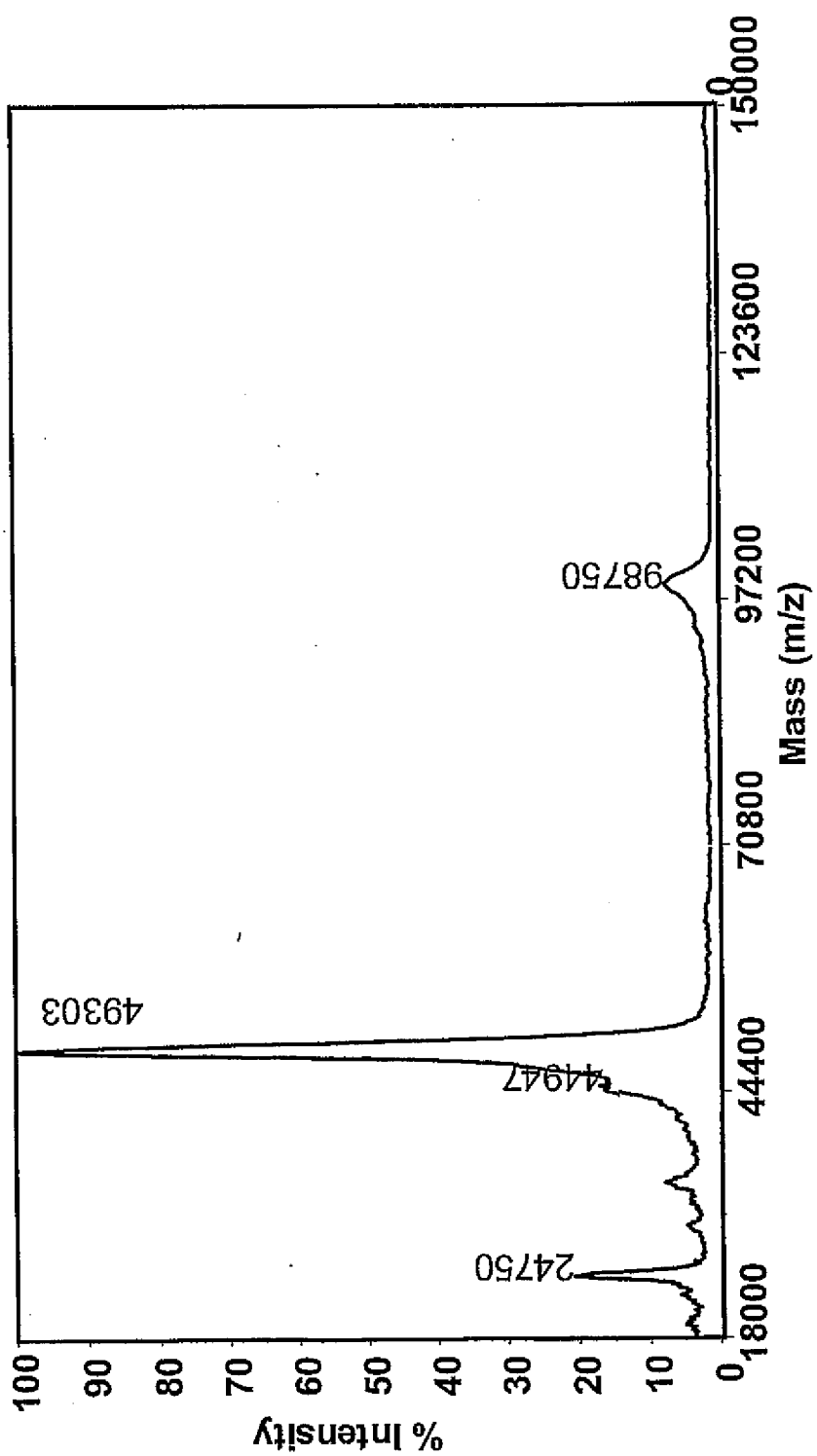


FIG. 117

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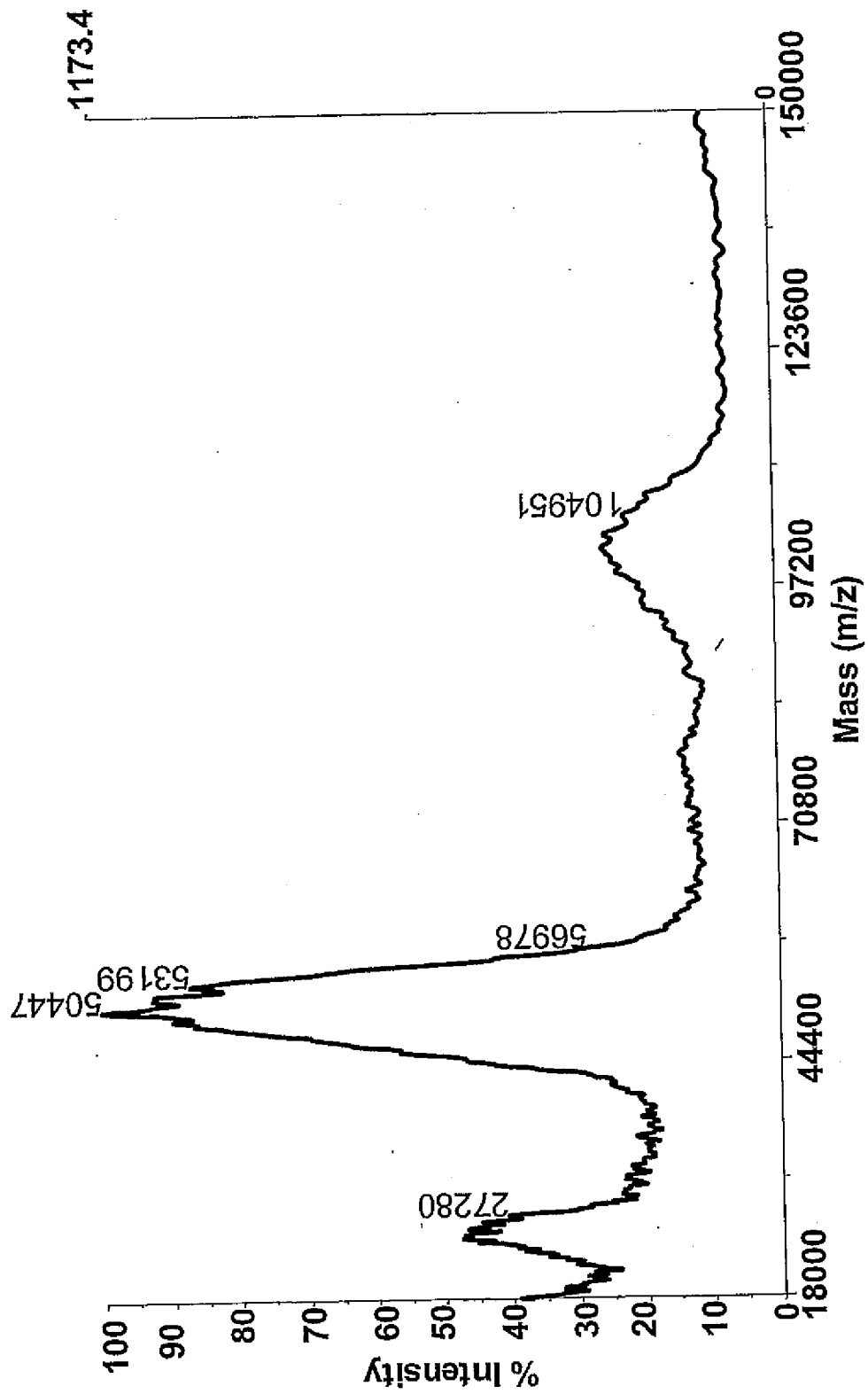


FIG. 118

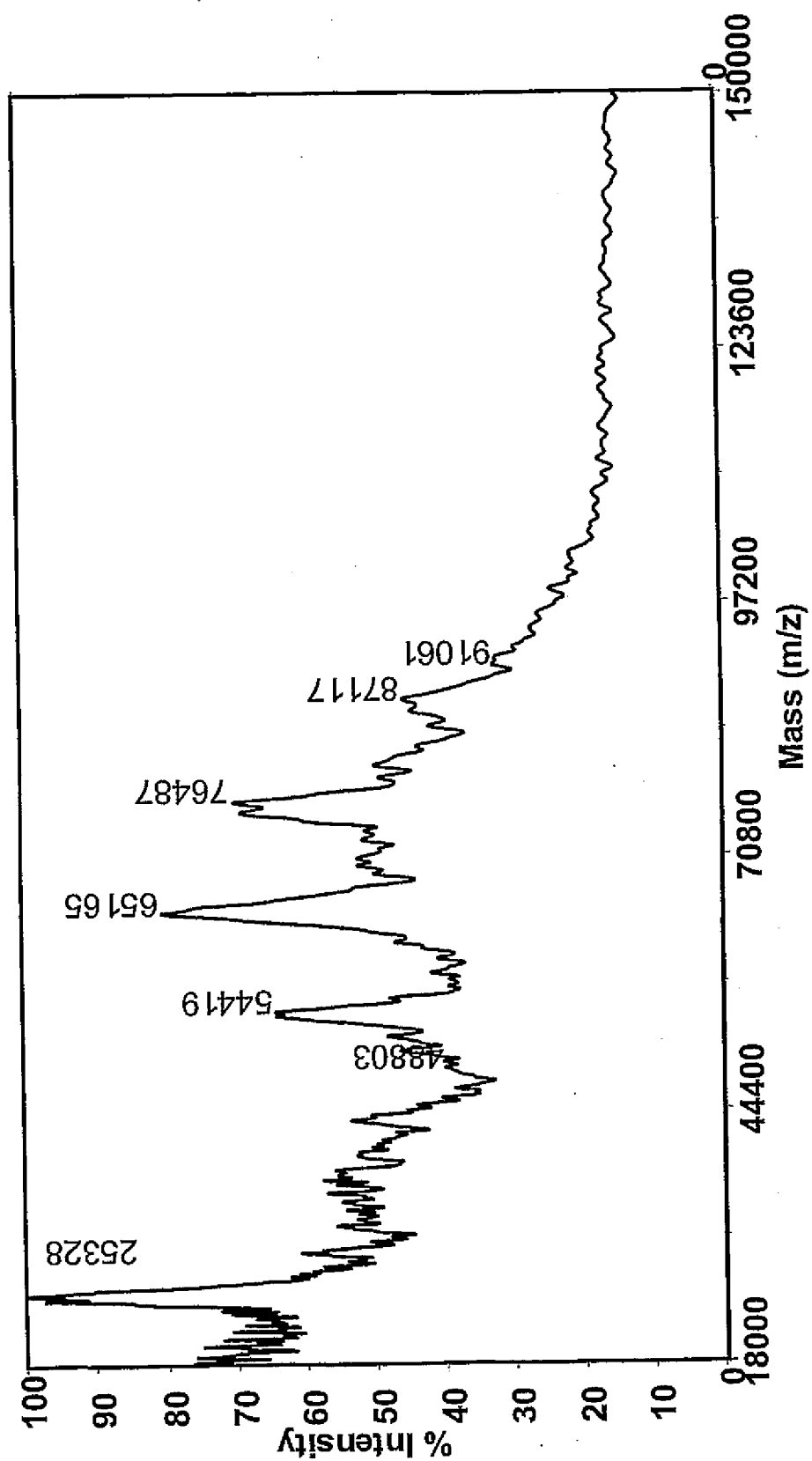


FIG. 119

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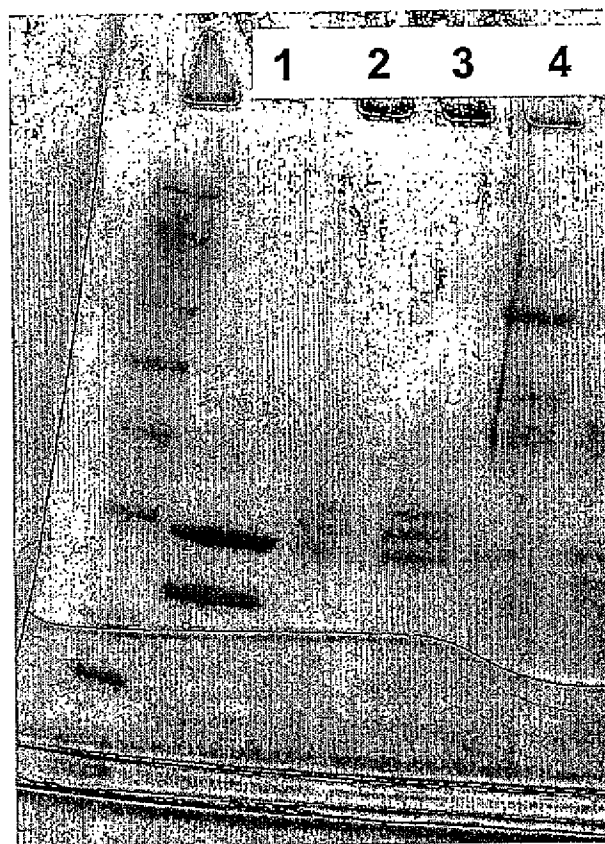


FIG. 120

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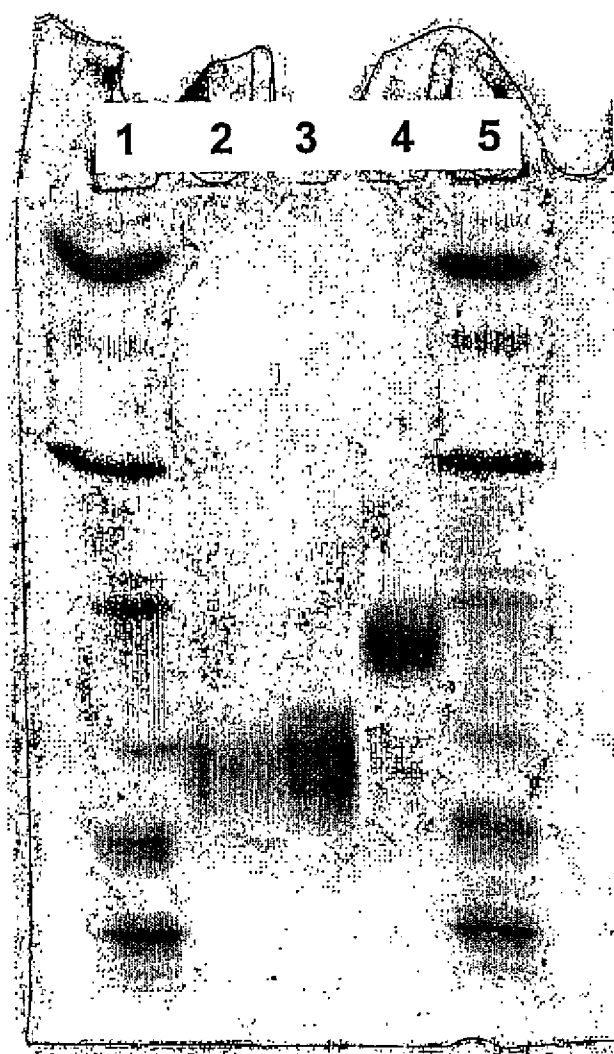


FIG. 121

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FIG. 122

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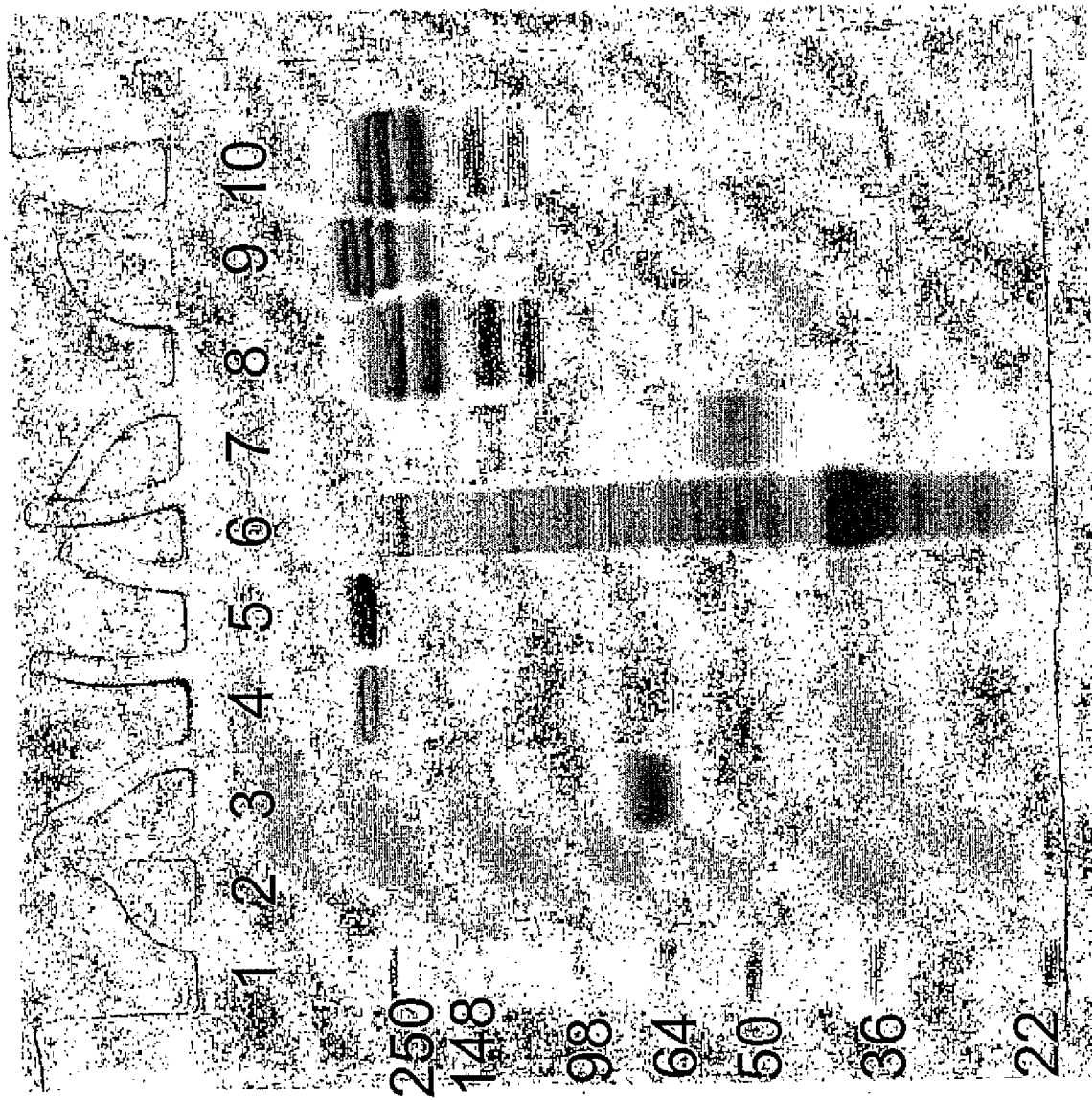


FIG. 123

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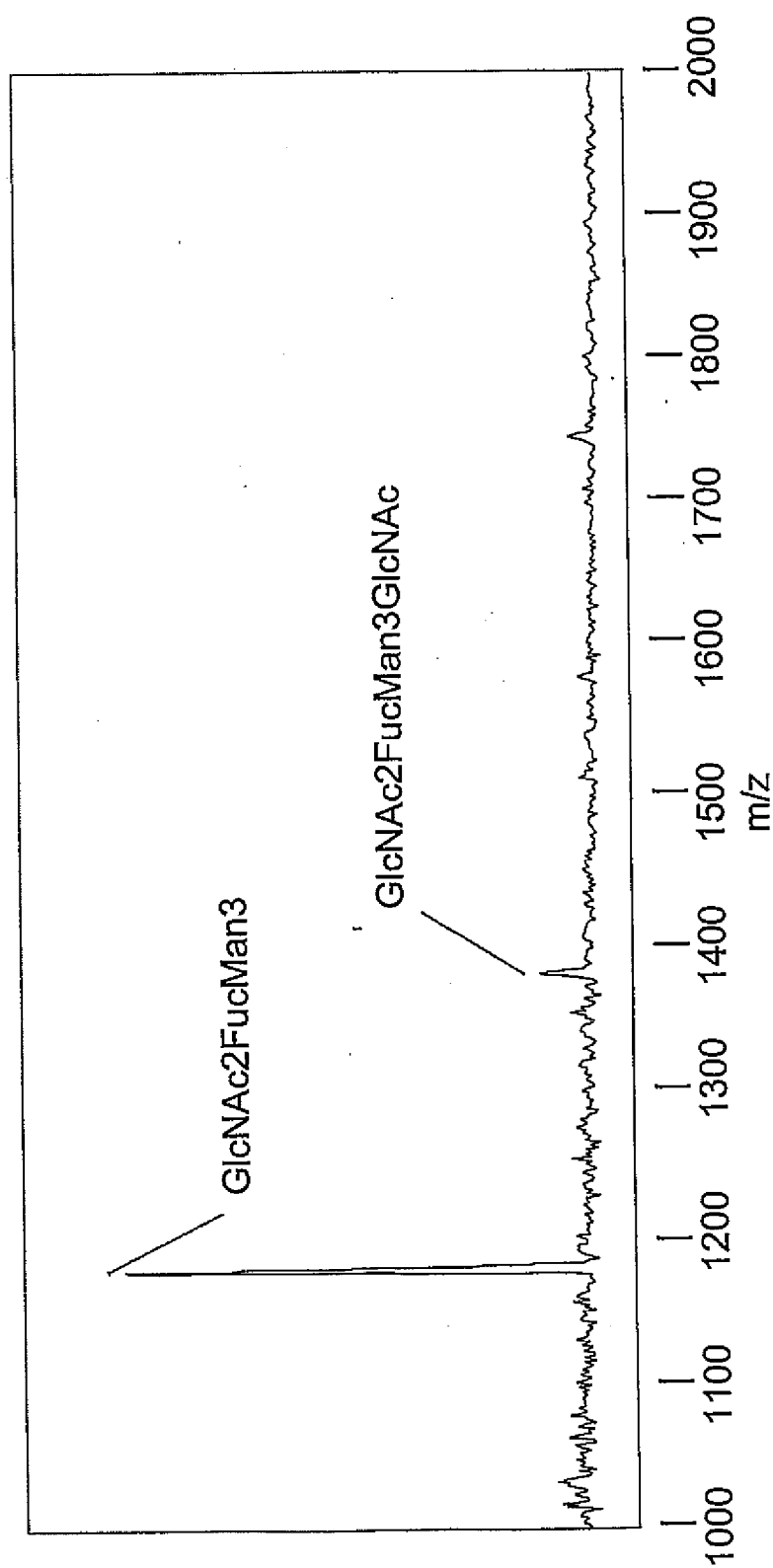


FIG. 124

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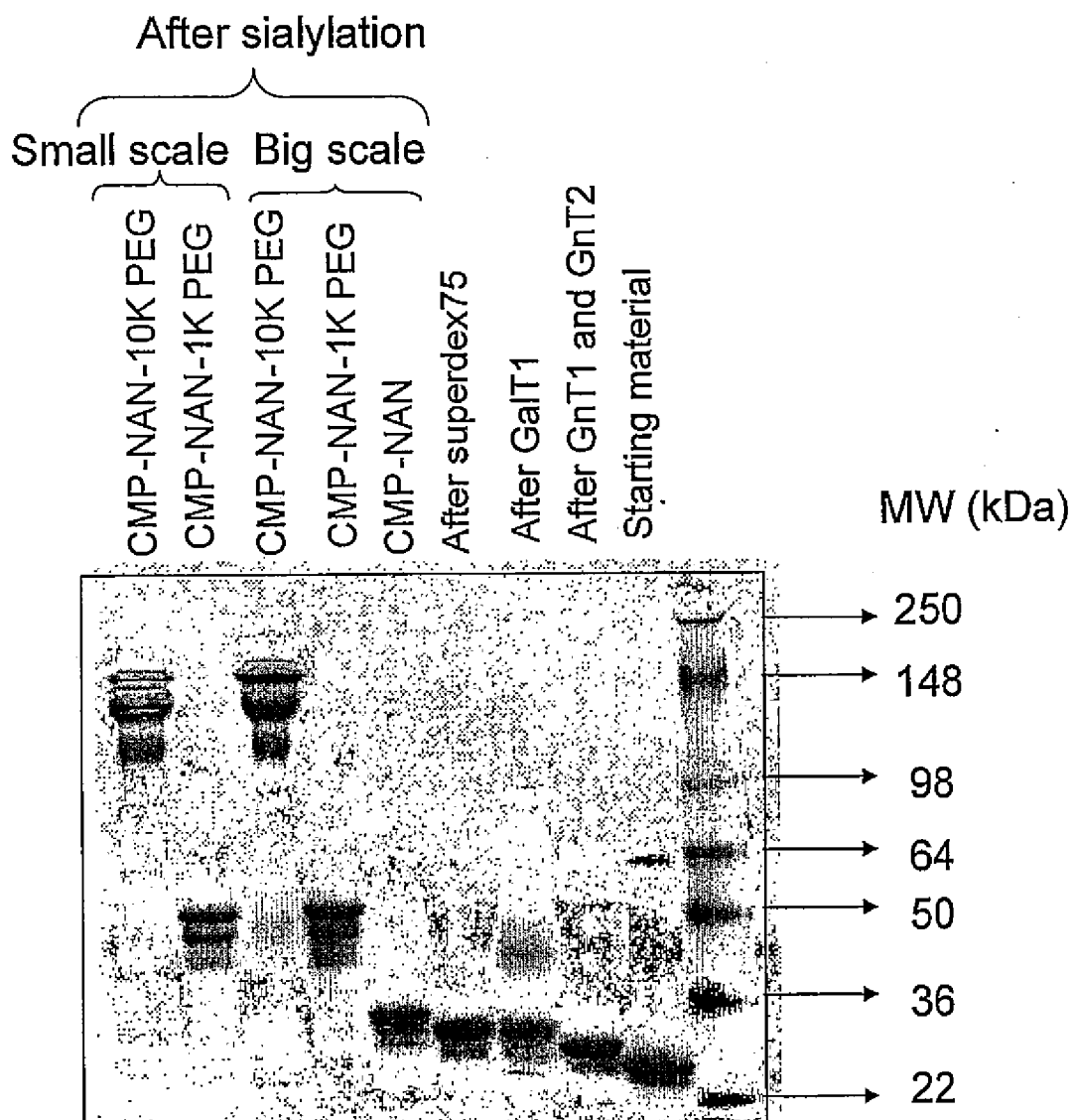


FIG. 125

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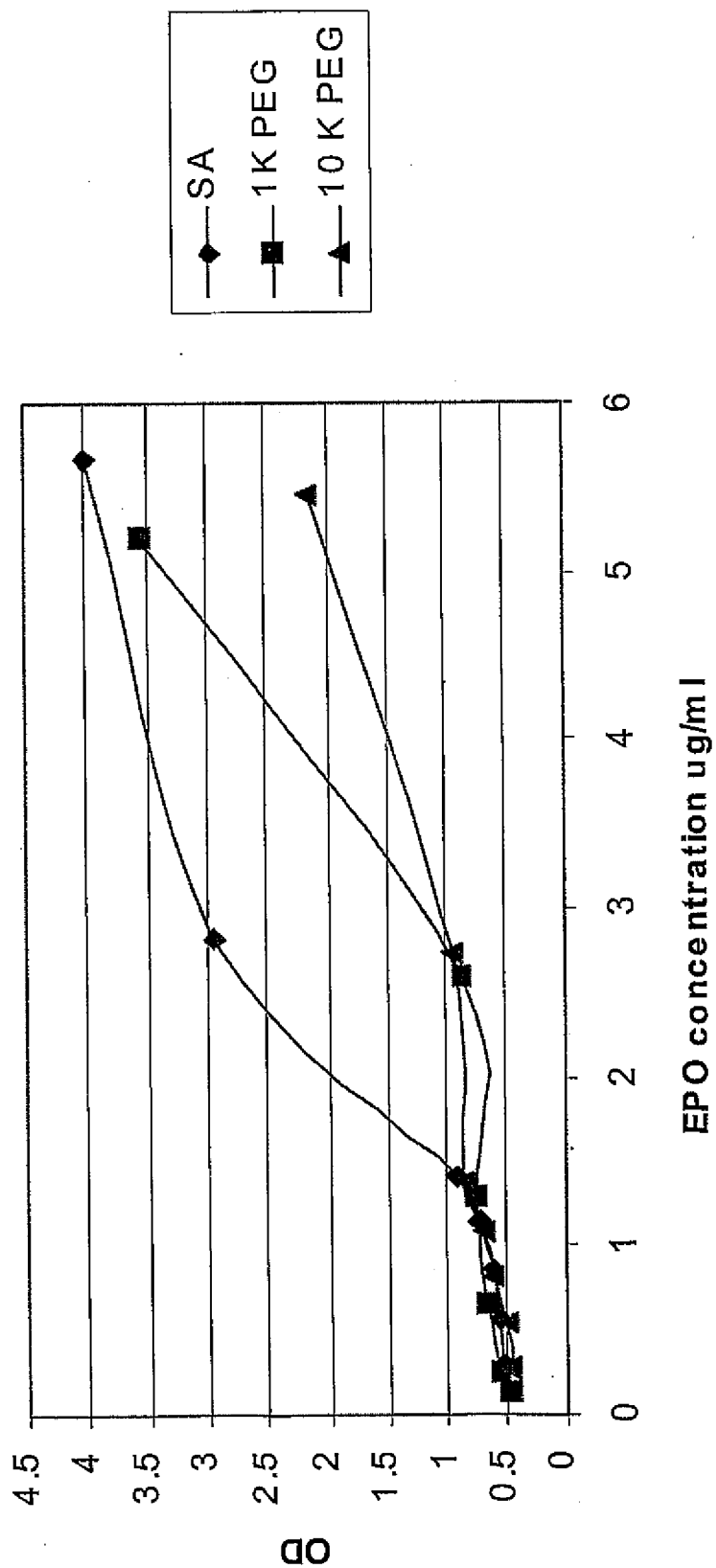


FIG. 126

SEQUENCE LISTING

<110> Neose Technologies, Inc.
 DeFrees, Shawn
 Zopf, David
 Bayer, Robert
 Bowe, Caryn
 Hakes, David
 Chen, Xi

<120> REMODELING AND GLYCOCONJUGATION OF PEPTIDES

<130> 040853-01-5050WO

<150> US 60/328,523

<151> 2001-10-10

<150> US 60/344,692

<151> 2001-10-19

<150> US 60/334,233

<151> 2001-11-08

<150> US 60/334,301

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<151> 2002-06-07

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<151> 2002-06-25

<150> US 60/396,594

<151> 2002-07-17

<150> US 60/404,249

<151> 2002-08-16

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<151> 2002-08-28

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ctgtgccacc ccgaggagct ggtgctgctc ggacactctc tgggcatccc ctgggctccc 180

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 cccaccttgg acacactgca gctggacgtc gccgactttg ccaccacat ctggcagcag 360
 atggaagaac tgggaatggc cctgcccctg cagcccaccc aggggtgcat gccggccttc 420
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<210> 2
 <211> 174
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 <213> Homo sapiens

<400> 2

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 1 5 10 15

Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe

145

150

155

160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 165 170

<210> 3

<211> 1733

<212> DNA

<213> Homo sapiens

<400> 3

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 tgcaataata aaacattaac ttatactttt ttaatttaat gtatagaata gagatataca 180
 taggatatgt aaatagatac acagtgtata tgtgattaaa atataatggg agattcaatc 240
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 tcctgcttga aggacagaca tgactttgga tttccccagg aggagtgttg caaccagttc 720
 caaaaggctg aaaccatccc tgtcctccat gagatgatcc agcagatctt caatctcttc 780
 agcaciaaagg actcatctgc tgcttgggat gagaccctcc tagacaaatt ctacactgaa 840
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 actcccctga tgaaggagga ctccattctg gctgtgagga aatacttcca aagaatcact 960
 ctctatctga aagagaagaa atacagccct tgtgcttggg aggttgtcag agcagaaatc 1020
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 1 5 10 15

Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
 20 25 30

Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
 35 40 45

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
 50 55 60

Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
 65 70 75 80

Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
 85 90 95

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
 100 105 110

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
 115 120 125

Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
 130 135 140

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
 165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
 180 185

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 tccatgagct acaacttgct tggattccta caaagaagca gcaattttca gtgtcagaag 120
 ctctgttggc aattgaatgg gaggcttgaa tattgcctca aggacaggat gaactttgac 180
 atccctgagg agattaagca gctgcagcag ttccagaagg aggacgccgc attgaccatc 240
 tatgagatgc tccagaacat ctttgctatt ttcagacaag attcatctag cactgggtgg 300
 aatgagacta ttgttgagaa cctcctggct aatgtctatc atcagataaa ccatctgaag 360
 acagtcctgg aagaaaaact ggagaaagaa gattttacca ggggaaaact catgagcagt 420
 ctgcacctga aaagatatta tgggaggatt ctgcattacc tgaaggccaa ggagtacagt 480
 cactgtgcct ggaccatagt cagagtggaa atcctaagga acttttactt cattaacaga 540
 cttacaggtt acctccgaaa ctgaagatct cctagcctgt ccctctggga ctggacaatt 600
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<210> 6
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 6

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 1 5 10 15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
 20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
 145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
 165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 180 185

<210> 7
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 <213> Homo sapiens

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 gcgcttcttg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc 180
 tccttcgagg aggcccgga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240

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gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggcog gaactgtgag   360
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gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa   540
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cggcggtgtg cgaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac   840
atgcgctgc tccgcctgca ccagcccggtg gtccctactg accatgtggt gcccctctgc   900
ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc   960
ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt gctcaacgtg  1020
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agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag  1260
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gccccatttc cc                                     1332

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<210> 8
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 8

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Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
1           5           10          15

```

```

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20          25          30

```

```

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35          40          45

```

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
 50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
 85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
 100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
 115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
 130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
 145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
 165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
 180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
 195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
 210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
 225 230 235 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
 245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
 260 265 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
 420 425 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
 435 440

<210> 9
 <211> 1437
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 ggatatctac tcagtgtga atgtacagtt tttcttgatc atgaaaacgc caacaaaatt 120
 ctgaatcggc caaagaggta taattcaggt aaattggaag agtttggtca aggggaacott 180

gagagagaat gtatggaaga aaagtgtagt tttgaagaac cactgagaagt ttttgaaaac 240
 actgaaaaga caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat 300
 ccatgtttta atggcggcag ttgcaaggat gacattaatt cctatgaatg ttggtgtccc 360
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 caggttgttt tgaatggtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa 780
 tggattgtaa ctgctgcccc ctgtgttgaa actgggtgta aaattacagt tgcgcaggt 840
 gaacataata ttgaggagac agaacataca gagcaaaaagc gaaatgtgat tcgagcaatt 900
 attcctcacc acaactacaa tgcagctatt aataagtaca accatgacat tgcccttctg 960
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 gaatacacga acatcttcct caaatttggg tctggctatg taagtggctg ggcaagagtc 1080
 ttccacaaag ggagatcagc tttagttctt cagtacctta gagttccact tgttgaccga 1140
 gccacatgtc ttgatctac aaagttcacc atctataaca acatgttctg tgctggcttc 1200
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 aaatatggaa tatataccaa ggtatccogg tatgtcaact ggattaagga aaaaacaaag 1380
 ctcaactaat gaaagatgga ttccaaggt taattcattg gaattgaaaa ttaacag 1437

<210> 10
 <211> 462
 <212> PRT
 <213> Homo sapiens

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 1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
 20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
 35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
 50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn
 65 70 75 80

Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
 85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
 100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
 115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
 130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
 145 150 155 160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
 165 170 175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
 180 185 190

Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu
 195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe
 210 215 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
 225 230 235 240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
 245 250 255

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His
 290 295 300

Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu
 305 310 315 320

Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys
 325 330 335

Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
 340 345 350

Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu
 355 360 365

Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu
 370 375 380

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
 450 455 460

<210> 11
 <211> 603
 <212> DNA
 <213> Homo sapiens

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ttctttctccc agccgggtgc cccaatactt cagtgcattgg gctgctgctt ctctagagca      180
tatcccactc cactaagggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag      240
tccacttgct gtgtagctaa atcatataac agggtcacag taatggggggg tttcaaagtg      300
gagaaccaca cggcgtgcc a ctgcagtact tgttattatc acaaatctta aatgttttac      360
caagtgtgtg cttgatgact gctgattttc tggaatggaa aattaagttg tttagtgttt      420
atggctttgt gagataaaac tctccttttc cttaccatac cactttgaca cgcttcaagg      480
atatactgca gctttactgc cttcctcctt atcctacagt acaatcagca gtctagttct      540
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atc                                                                    603

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<210> 12
<211> 116
<212> PRT
<213> Homo sapiens

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<400> 12
Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1          5          10          15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
          20          25          30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
          35          40          45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
          50          55          60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65          70          75          80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
          85          90          95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
          100          105          110

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Tyr His Lys Ser
115

<210> 13
<211> 390
<212> DNA
<213> Homo sapiens

<400> 13
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atcaacacca cttgggtgtgc tggctactgc tacaccaggg atctgggtgta taaggaccca 180
gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggatatatga aacagtgaga 240
gtgcccggct gtgctcacca tgcagattcc ttgtatacat acccagtggc caccagtgt 300
cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggccagc 360
tactgctcct ttgggtgaaat gaaagaataa 390

<210> 14
<211> 129
<212> PRT
<213> Homo sapiens

<400> 14

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
 100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys
 115 120 125

Glu

<210> 15
 <211> 1342
 <212> DNA
 <213> Homo sapiens

<400> 15
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 gcccccggtg tggtcacccg gcgcgcccga ggtcgctgag ggaccccggc caggcgcgga 180
 gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgctccc 240
 totgggcctc ccagtcctgg gcgccccacc acgcctcctc tgtgacagcc gagtcctgga 300
 gaggtacctc ttggaggcca aggaggccga gaatatcaag acgggctgtg ctgaacactg 360
 cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag 420
 gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc 480
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 cactgctgac actttccgca aactcttcg agtctactcc aatttcctcc ggggaaagct 720
 gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccagggtg tgtccacctg 780
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 gcaatgacat ctccaggggc agaggaactg tccagagagc aactctgaga tctaaggatg 960
 tcacagggcc aacttgaggg ccagagcag gaagcattca gagagcagct ttaaactcag 1020
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 aggacacgct ttggaggcga ttacctggt ttcgcaccta ccatcaggga caggatgacc 1140

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tggagaactt aggtggcaag ctgtgacttc tccaggtctc acgggcatgg gcactccctt 1200
gggtggcaaga gcccccttga caccgggggtg gtgggaacca tgaagacagg atgggggctg 1260
gcctctgggt ctcatgggggt ccaagttttg tgtattcttc aacctcattg acaagaactg 1320
aaaccaccaa aaaaaaaaaa aa 1342

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<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

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<400> 16

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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1           5           10           15

```

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Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
          20           25           30

```

```

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
          35           40           45

```

```

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50           55           60

```

```

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65           70           75           80

```

```

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
          85           90           95

```

```

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100           105           110

```

```

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115           120           125

```

```

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
130           135           140

```

```

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145           150           155           160

```

```

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu

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165

170

175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Arg

<210> 17
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 17
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 cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcac 180
 tcagaaatgt ttgacctcca ggagccgacc tgcctacaga cccgcctgga gctgtacaag 240
 cagggcctgc ggggcagcct caccaagctc aaggggccct tgaccatgat ggccagccac 300
 tacaagcagc actgcctcc aaccccgga acttctctgtg caaccagat tatcacottt 360
 gaaagtttca aagagaacct gaaggacttt ctgcttgtca tcccctttga ctgctgggag 420
 ccagtccagg agtga 435

<210> 18
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
 1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
 20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
 35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
 50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
130 135 140

<210> 19
<211> 501
<212> DNA
<213> Homo sapiens

<400> 19
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tgttactgcc aggaccata tgtaaaagaa gcagaaaacc ttaagaaata ttttaatgca 120
ggtcattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180
gaggagagt acagaaaaat aatgcagagc caaattgtct ccttttactt caaacttttt 240
aaaaacttta aagatgacca gagcatccaa aagagtgtgg agaccatcaa ggaagacatg 300
aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360
tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg 420
gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480
ggtcgaagag catcccagta a 501

<210> 20
<211> 166
<212> PRT
<213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu

20	25	30
Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn 35 40 45		
Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp 50 55 60		
Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe 65 70 75 80		
Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile 85 90 95		
Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg 100 105 110		
Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val 115 120 125		
Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser 130 135 140		
Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg 145 150 155 160		
Gly Arg Arg Ala Ser Gln 165		

<210> 21
 <211> 1352
 <212> DNA
 <213> Homo sapiens

<400> 21
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 gacagataca tcccaccatg atcaggatca cccaaccttc aacaagatca cccccaacct 180
 ggctgagttc gccttcagcc tataccgcca gctggcacac cagtccaaca gcaccaatat 240
 cttcttctcc ccagttagca tcgctacagc ctttgcaatg ctctccctgg ggaccaaggc 300
 tgacactcac gatgaaatcc tggagggcct gaatttcaac' ctcacggaga ttccggaggc 360

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tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct 420
ccagctgacc accggcaatg gcctgttcct cagcgagggc ctgaagctag tggataagtt 480
tttggaggat gttaaaaagt tgtaccactc agaagccttc actgtcaact tcggggacac 540
cgaagaggcc aagaaacaga tcaacgatta cgtggagaag ggtactcaag ggaaaattgt 600
ggatttggtc aaggagcttg acagagacac agtttttgct ctggtgaatt acatcttctt 660
taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt 720
ggaccaggtg accaccgtga aggtgcctat gatgaagcgt ttaggcattgt ttaacatcca 780
gcactgtaag aagctgtcca gctgggtgct gctgatgaaa tacctgggca atgccaccgc 840
catcttcttc ctgcctgatg aggggaaact acagcacctg gaaaatgaac tcacccacga 900
tatcatcacc aagttcctgg aaaatgaaga cagaaggtct gccagettac atttacccaa 960
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ggtcttcagc aatggggctg acctctccgg ggtcacagag gaggcacccc tgaagctctc 1080
caaggccgtg cataaggctg tgctgaccat cgacgagaaa gggactgaag ctgctggggc 1140
catgttttta gaggccatac ccatgtctat ccccccgag gtcaagttca acaaaccctt 1200
tgtcttctta atgattgaac aaaataccaa gtctcccctc ttcattgggaa aagtggtgaa 1260
tcccacccaa aaataactgc ctctcgctcc tcaacccctc ccctccatcc ctggccccct 1320
ccctggatga cattaaagaa gggttgagct gg 1352

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<210> 22
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
 1 5 10 15

Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
 20 25 30

Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 35 40 45

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 50 55 60

Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 65 70 75 80

Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 85 90 95

His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
 100 105 110

Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 115 120 125

Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 145 150 155 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 165 170 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 180 185 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 195 200 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 210 215 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
 225 230 235 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 245 250 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 260 265 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 275 280 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 290 295 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 305 310 315 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 325 330 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 355 360 365

Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 370 375 380

Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 385 390 395 400

Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 405 410 415

Gln Lys

<210> 23
 <211> 2004
 <212> DNA
 <213> Homo sapiens

<400> 23
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 ggatggagtt ttcaagtcct tccagagagg aatgtcccaa gcctttgagt agggtaagca 180
 tcatggctgg cagocctaca gggttgcttc tacttcaggc agtgcgtgg gcatcaggtg 240
 cccgcccctg catocctaaa agcttcggct acagctcggg ggtgtgtgtc tgcaatgcca 300
 catactgtga ctcttttgac ccccgacct ttctgcctc tggtaacctc agccgctatg 360
 agagtacacg cagtgggcca cggatggagg tgagtatggg gccatccag gctaatacaca 420
 cgggacacagg cctgctactg acctgcagc cagaacagaa gttccagaaa gtgaagggat 480

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ttggagggggc catgacagat gctgctgctc tcaacatcct tgccctgtca cccctgccc      540
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taccatggc cagctgtgac ttctccatcc gcacctacac ctatgcagac acccctgatg      660
atttccagtt gcacaacttc agcctcccag aggaagatac caagctcaag ataccctga      720
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caccacttg gctcaagacc aatggagcgg tgaatgggaa ggggtcactc aaggacagc      840
ccggagacat ctaccaccag acctgggcca gatactttgt gaagtctctg gatgcctatg      900
ctgagcaciaa gttacagttc tgggcagtga cagctgaaaa tgagccttct gctgggctgt      960
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aagccaccct aggggagaca caccgcctgt tccccaacac catgctcttt gcctcagagg     1260
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ggggcaatgg tttgggtgac tcactttccc ctctaggtgg tgcccagggc tggaggcccc     1920
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<210> 24
<211> 536
<212> PRT

<213> Homo sapiens

<400> 24

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
 1 5 10 15

Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
 20 25 30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
 65 70 75 80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
 85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu

[illegible]

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
 465 470 475 480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
 500 505 510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp His Arg Gln
 530 535

<210> 25
 <211> 1726
 <212> DNA
 <213> Homo sapiens

<400> 25
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 tgcagagatg aaaaaacgca gatgatatac cagcaacatc agtcatggct gcgcccctgtg 180
 ctcagaagca accgggtgga atattgctgg tgcaacagtg gcagggcaca gtgccactca 240
 gtgcctgtca aaagttgcag cgagccaagg tgtttcaacg ggggcacctg ccagcaggcc 300
 ctgtacttct cagatttcgt gtgccagtgc cccgaaggat ttgctgggaa gtgctgtgaa 360
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 acagcggaga gtggcgccga gtgcaccaac tggaacagca gcgcgttggc ccagaagccc 480
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 tcagcctacc gtggcacgca cagcctcacc gagtcgggtg cctcctgcct cccgtggaat 720
 tccatgatcc tgataggcaa ggtttacaca gcacagaacc ccagtgccca ggcactgggc 780

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ctgagacagt acagccagcc tcagtttcgc atcaaaggag ggctcttcgc cgacatcgcc      960
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gagaggtttc cgccccacca cctgacggtg atcttgggca gaacataccg ggtggtccct     1140
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gacacttacg acaatgacat tgcgctgctg cagctgaaat cggattcgtc ccgctgtgcc     1260
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tggacggagt gtgagctctc cggtacggc aagcatgagg ccttgtctcc ttctattcg     1380
gagcggctga aggaggctca tgtcagactg taccatcca gccgctgcac atcacaacat     1440
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aacgatggcc gcatgacttt ggtgggcatc atcagctggg gcctgggctg tggacagaag     1620
gatgtcccg gtgtgtacac caaggttacc aactacctag actggattcg tgacaacatg     1680
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<210> 26
 <211> 562
 <212> PRT
 <213> Homo sapiens

<400> 26

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
          20           25           30

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Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
35           40           45

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Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
50           55           60

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Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65 70 75 80

Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
85 90 95

Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
100 105 110

Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
115 120 125

Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
130 135 140

Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
145 150 155 160

Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
165 170 175

Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
180 185 190

Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
195 200 205

Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
210 215 220

Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
225 230 235 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
245 250 255

Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
260 265 270

Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
275 280 285

Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr

290	295	300
Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala		
305	310	315 320
Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro		
	325	330 335
Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile		
	340	345 350
Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu		
	355	360 365
Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu		
	370	375 380
Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp		
385	390	395 400
Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser		
	405	410 415
Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro		
	420	425 430
Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly		
	435	440 445
Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys		
	450	455 460
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His		
465	470	475 480
Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr		
	485	490 495
Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp		
	500	505 510
Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val		
	515	520 525

Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
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Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
 545 550 555 560

Arg Pro

<210> 27
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 27
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 ccagggactt aatcagcaat atcaacgtaa tagttctgga actaaaggga tctgaaacaa 420
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<210> 28
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 28

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<210> 30
 <211> 2351
 <212> PRT
 <213> Homo sapiens

<400> 30

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
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```

Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
          20           25           30

```

```

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
          35           40           45

```

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Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
          50           55           60

```

```

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65           70           75           80

```

```

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
          85           90           95

```

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
 100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
 115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
 130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
 145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
 165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
 180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
 195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
 210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
 225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
 245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
 260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
 275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
 290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
 305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
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Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
 340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
 355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
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Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
 385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
 405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
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Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
 435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
 450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
 465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
 485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
 500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
 515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
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Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg

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Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu			
	565	570	575
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	580	585	590
Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu			
	595	600	605
Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp			
	610	615	620
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val			
	625	630	635
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp			
	645	650	655
Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe			
	660	665	670
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr			
	675	680	685
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro			
	690	695	700
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly			
	705	710	715
Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp			
	725	730	735
Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys			
	740	745	750
Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg			
	755	760	765
Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp			
	770	775	780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
785 790 795 800

Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
805 810 815

Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
820 825 830

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
835 840 845

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
850 855 860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
865 870 875 880

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
885 890 895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
900 905 910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
915 920 925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
930 935 940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
945 950 955 960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
965 970 975

Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
980 985 990

Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
995 1000 1005

Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser
 1010 1015 1020

Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser
 1025 1030 1035

Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu
 1040 1045 1050

Ser Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg
 1055 1060 1065

Met Leu Met Asp Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met
 1070 1075 1080

Ser Asn Lys Thr Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln
 1085 1090 1095

Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met
 1100 1105 1110

Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile
 1115 1120 1125

Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro
 1130 1135 1140

Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu
 1145 1150 1155

Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys
 1160 1165 1170

Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe Pro
 1175 1180 1185

Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu
 1190 1195 1200

Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu
 1205 1210 1215

Lys	Lys	Glu	Thr	Leu	Ile	Gln	Glu	Asn	Val	Val	Leu	Pro	Gln	Ile
1220						1225					1230			
His	Thr	Val	Thr	Gly	Thr	Lys	Asn	Phe	Met	Lys	Asn	Leu	Phe	Leu
1235						1240					1245			
Leu	Ser	Thr	Arg	Gln	Asn	Val	Glu	Gly	Ser	Tyr	Asp	Gly	Ala	Tyr
1250						1255					1260			
Ala	Pro	Val	Leu	Gln	Asp	Phe	Arg	Ser	Leu	Asn	Asp	Ser	Thr	Asn
1265						1270					1275			
Arg	Thr	Lys	Lys	His	Thr	Ala	His	Phe	Ser	Lys	Lys	Gly	Glu	Glu
1280						1285					1290			
Glu	Asn	Leu	Glu	Gly	Leu	Gly	Asn	Gln	Thr	Lys	Gln	Ile	Val	Glu
1295						1300					1305			
Lys	Tyr	Ala	Cys	Thr	Thr	Arg	Ile	Ser	Pro	Asn	Thr	Ser	Gln	Gln
1310						1315					1320			
Asn	Phe	Val	Thr	Gln	Arg	Ser	Lys	Arg	Ala	Leu	Lys	Gln	Phe	Arg
1325						1330					1335			
Leu	Pro	Leu	Glu	Glu	Thr	Glu	Leu	Glu	Lys	Arg	Ile	Ile	Val	Asp
1340						1345					1350			
Asp	Thr	Ser	Thr	Gln	Trp	Ser	Lys	Asn	Met	Lys	His	Leu	Thr	Pro
1355						1360					1365			
Ser	Thr	Leu	Thr	Gln	Ile	Asp	Tyr	Asn	Glu	Lys	Glu	Lys	Gly	Ala
1370						1375					1380			
Ile	Thr	Gln	Ser	Pro	Leu	Ser	Asp	Cys	Leu	Thr	Arg	Ser	His	Ser
1385						1390					1395			
Ile	Pro	Gln	Ala	Asn	Arg	Ser	Pro	Leu	Pro	Ile	Ala	Lys	Val	Ser
1400						1405					1410			
Ser	Phe	Pro	Ser	Ile	Arg	Pro	Ile	Tyr	Leu	Thr	Arg	Val	Leu	Phe
1415						1420					1425			
Gln	Asp	Asn	Ser	Ser	His	Leu	Pro	Ala	Ala	Ser	Tyr	Arg	Lys	Lys

1430	1435	1440
Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys		
1445	1450	1455
Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly		
1460	1465	1470
Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser		
1475	1480	1485
Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp		
1490	1495	1500
Leu Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His		
1505	1510	1515
Ile Tyr Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser		
1520	1525	1530
Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr		
1535	1540	1545
Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val		
1550	1555	1560
Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser		
1565	1570	1575
Lys Leu Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln		
1580	1585	1590
Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys		
1595	1600	1605
Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys		
1610	1615	1620
Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys		
1625	1630	1635
Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg		
1640	1645	1650

Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu	1655	1660	1665
Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr	1670	1675	1680
Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile	1685	1690	1695
Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys	1700	1705	1710
Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr	1715	1720	1725
Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser	1730	1735	1740
Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr	1745	1750	1755
Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu	1760	1765	1770
His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp	1775	1780	1785
Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser	1790	1795	1800
Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly	1805	1810	1815
Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr	1820	1825	1830
Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu	1835	1840	1845
Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu	1850	1855	1860

Lys	Asp	Val	His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His
1865						1870					1875			
Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln
1880						1885					1890			
Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp
1895						1900					1905			
Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn
1910						1915					1920			
Ile	Gln	Met	Glu	Asp	Pro	Thr	Phe	Lys	Glu	Asn	Tyr	Arg	Phe	His
1925						1930					1935			
Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp	Thr	Leu	Pro	Gly	Leu	Val	Met
1940						1945					1950			
Ala	Gln	Asp	Gln	Arg	Ile	Arg	Trp	Tyr	Leu	Leu	Ser	Met	Gly	Ser
1955						1960					1965			
Asn	Glu	Asn	Ile	His	Ser	Ile	His	Phe	Ser	Gly	His	Val	Phe	Thr
1970						1975					1980			
Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met	Ala	Leu	Tyr	Asn	Leu	Tyr
1985						1990					1995			
Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met	Leu	Pro	Ser	Lys	Ala	Gly
2000						2005					2010			
Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly	Glu	His	Leu	His	Ala	Gly
2015						2020					2025			
Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser	Asn	Lys	Cys	Gln	Thr	Pro
2030						2035					2040			
Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile	Thr	Ala
2045						2050					2055			
Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro	Lys	Leu	Ala	Arg	Leu	His
2060						2065					2070			

Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	Phe	Ser
2075						2080					2085			
Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile
2090						2095					2100			
Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr	Ile	Ser
2105						2110					2115			
Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	Gln	Thr
2120						2125					2130			
Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn
2135						2140					2145			
Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile
2150						2155					2160			
Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	Thr	His	Tyr	Ser	Ile	Arg
2165						2170					2175			
Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	Cys	Asp	Leu	Asn	Ser	Cys
2180						2185					2190			
Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	Ala	Ile	Ser	Asp	Ala	Gln
2195						2200					2205			
Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn	Met	Phe	Ala	Thr	Trp	Ser
2210						2215					2220			
Pro	Ser	Lys	Ala	Arg	Leu	His	Leu	Gln	Gly	Arg	Ser	Asn	Ala	Trp
2225						2230					2235			
Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys	Glu	Trp	Leu	Gln	Val	Asp	Phe
2240						2245					2250			
Gln	Lys	Thr	Met	Lys	Val	Thr	Gly	Val	Thr	Thr	Gln	Gly	Val	Lys
2255						2260					2265			
Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	Ser	Ser
2270						2275					2280			
Ser	Gln	Asp	Gly	His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	Gly	Lys

2285 2290 2295
 Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val
 2300 2305 2310
 Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His
 2315 2320 2325
 Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu
 2330 2335 2340
 Gly Cys Glu Ala Gln Asp Leu Tyr
 2345 2350

<210> 31
 <211> 1471
 <212> DNA
 <213> Homo sapiens

<400> 31
 atggcgccccg tcgccgtctg ggccgcgctg gccgtcggac tggagctctg ggctgcggcg 60
 cacgccttgc cgcgccaggt ggcatttaca ccctacgccc cggagcccgg gagcacatgc 120
 cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaattg ctgcgcgggc 180
 caacatgcaa aagtcttctg taccaagacc tcggacacog tgtgtgactc ctgtgaggac 240
 agcacatata ccagctctg gaactgggtt cccgagtgtg tgagctgtgg ctcccgtgtg 300
 agctctgacc aggtggaaac tcaagcctgc actcgggaac agaaccgcat ctgcacctgc 360
 aggcccggtt ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgcgcgcgtg 420
 cgcaagtgcc gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtgggtg 480
 tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgagg 540
 cccaccaga tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc 600
 acgtccacgt cccccaccg gagtatggcc ccaggggcag tacacttacc ccagccagtg 660
 tccacacgat cccaacacac gcagccaact ccagaacca gactgctcc aagcacctcc 720
 ttctgtctcc caatgggccc cagcccccca gctgaaggga gactggcga ctctgctctt 780
 ccagttggac tgattgtggg tgtgacagcc ttgggtctac taataatagg agtgggtgaac 840
 tgtgtcatca tgaccaggt gaaaaagaag cccttgtgcc tgcagagaga agccaagggtg 900
 cctcacttgc ctgccgataa ggccgggggt acacagggcc ccgagcagca gcacctgctg 960

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atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga 1020
agggcgccca ctcggaacca gccacaggca ccaggcgtgg aggccagtgg ggccggggag 1080
ggccggggcca gcaccgggag ctccagattct tcccctgggtg gccatgggac ccagggtcaat 1140
gtcacctgca togtgaacgt ctgtagcagc tctgaccaca gctcacagtg ctctctccaa 1200
gccagctcca caatgggaga cacagattcc agcccctcgg agtccccgaa ggacgagcag 1260
gtcccccttct ccaaggagga atgtgccttt cggtcacagc tggagacgcc agagaccctg 1320
ctgggggagca ccgaagagaa gcccctgccc cttggagtgc ctgatgctgg gatgaagccc 1380
agttaaccag gccggtgtgg gctgtgtcgt agccaagggtg ggctgagccc tggcaggatg 1440
accctgcgaa ggggccctgg tccttccagg c 1471

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<210> 32
<211> 461
<212> PRT
<213> Homo sapiens

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```

<400> 32

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Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1           5           10           15

```

```

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
          20           25           30

```

```

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
          35           40           45

```

```

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50           55           60

```

```

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65           70           75           80

```

```

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
          85           90           95

```

```

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
          100           105           110

```

```

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
          115           120           125

```


Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335

Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
 420 425 430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
 435 440 445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
 450 455 460

<210> 33
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 33
 tccacctgtc cccgcagcgc cggctcgcgc cctcctgccg cagccaccga gccgcgctct 60
 agcgcgccga cctcgccacc atgagagccc tgctggcgcg cctgcttctc tgcgtcctgg 120
 tcgtgagcga ctccaaaggc agcaatgaac ttcattcaagt tccatcgaac tgtgactgtc 180
 taaatggagg aacatgtgtg tccaacaagt acttctccaa cattcactgg tgcaactgcc 240
 caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300
 atggtcactt ttaccgagga aaggccagca ctgacaccat gggccggccc tgccctgccct 360
 ggaactctgc cactgtcctt cagcaaacgt accatgccca cagatctgat gctcttcagc 420
 tgggcctggg gaaacataat tactgcagga acccagacaa ccggaggcga ccctggtgct 480
 atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcac ggtgcatgac tgcgcagatg 540
 gaaaaaagcc ctctctctct ccagaagaat taaaatttca gtgtggccaa aagactctga 600
 ggccccgctt taagattatt gggggagaat tcaccacccat cgagaaccag ccctgggttg 660
 cggccatcta caggaggcac cggggggggt ctgtcaccta cgtgtgtgga ggcagcctca 720

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tcagcccttg ctgggtgatc agcgccacac actgcttcat tgattacca aagaaggagg 780
actacatcgt ctacctgggt cgctcaaggc ttaactccaa cacgcaaggg gagatgaagt 840
ttgaggtgga aaacctcatc ctacacaagg actacagcgc tgacacgctt gctcaccaca 900
acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgag ccatcccga 960
ctatacagac catctgcctg cctcgatgt ataacgatcc ccagtttggc acaagctgtg 1020
agatcactgg ctttggaaaa gagaattcta ccgactatct ctatccggag cagctgaaga 1080
tgactgttgt gaagctgatt tcccaccggg agtgtcagca gcccactac tacggctctg 1140
aagtcaccac caaaatgctg tgtgctgctg acccacagtg gaaaacagat tcctgccagg 1200
gagactcagg gggaccctc gtctgttccc tccaaggcgc catgactttg actggaattg 1260
tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac 1320
acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggg 1380
ccccagggag gaaacgggca ccaccgctt tcttgctggt tgtcattttt gcagtagagt 1440
catctccatc agctgtaaga agagactggg aagat 1475

```

```

<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

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```

<400> 34

```

```

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1           5           10           15

```

```

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
          20           25           30

```

```

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
          35           40           45

```

```

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
          50           55           60

```

```

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65           70           75           80

```

```

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
          85           90           95

```

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
 180 185 190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
 195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
 210 215 220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
 225 230 235 240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
 245 250 255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
 260 265 270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
 275 280 285

Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
 290 295 300

Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
 305 310 315 320

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 36
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 37
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 37

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 38
 <211> 106
 <212> PRT
 <213> Mus musculus

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 39
 <211> 1039
 <212> DNA
 <213> Homo sapiens

<400> 39
 tctctgcacag gcagtgcctt gaagtgcttc ttcagagacc tttcttcata gactactttt 60
 tttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120
 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg 180
 ggggcgctgc tggcactggc ggccctactg caggggggccc tgtccctgaa gatcgcagcc 240
 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 300
 gtgcagatcc tgagccgcta tgacatgcc ctggtccagg aggtcagaga cagccacctg 360
 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420
 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480
 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgoga gccctgcggg 540
 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgggt cacagaggtc 600
 agggagtttg ccattgttcc cctgcatgcg gcccgggggg acgcagtagc cgagatcgac 660
 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg 720
 atgggcgact tcaatgcggg ctgcagctat gtgagacctt ccagtggtc atccatccgc 780
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<210> 40
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu

1	5	10	15
Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr	20	25	30
Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val	35	40	45
Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp	50	55	60
Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp	65	70	75
Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn	85	90	95
Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser	100	105	110
Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn	115	120	125
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe	130	135	140
Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly	145	150	155
Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val	165	170	175
Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn	180	185	190
Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu	195	200	205
Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr	210	215	220
Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly	225	230	235
			240

20	25	30
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile 35 40 45		
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly 50 55 60		
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser 65 70 75 80		
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe 85 90 95		
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu 100 105 110		
Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser 115 120 125		
Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val 130 135 140		
Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser 145 150 155 160		
Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg 165 170 175		
Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met 180 185 190		
Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn 195 200 205		
Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr 210 215 220		
Val Ser 225		
<210> 43		
<211> 450		

<212> DNA

<213> Homo sapiens

<400> 43

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gctgcatcag aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc      60
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tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaac      180
gaggcttctt ctacacaccc aagaccgccc gggaggcaga ggacctgcag gtggggcagg      240
tggagctggg cggggggcct ggtgcaggca gcctgcagcc cttggccctg gaggggtccc      300
tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg      360
agaactactg caactagacg cagcccgagc gcagccccc acccgccgcc tcttgcaccc      420
agagagatgg aataaagccc ttgaaccagc      450

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<210> 44

<211> 110

<212> PRT

<213> Homo sapiens

<400> 44

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Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1           5           10           15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
          20           25           30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
          35           40           45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
          50           55           60

Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65           70           75           80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
          85           90           95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
          100          105          110

```

<210> 45

<211> 1203
 <212> DNA
 <213> Hepatitis B virus

<400> 45
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 ccagattggg acttcaaccc caacaaggat cactggccag aggcaatcaa ggtaggagcg 180
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 gctcagggca tattgacaac agtgccagca ggcctcctc ctgtttccac caatcggcag 300
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 cagtggaaact ccacaacatt ccaccaagct ctgctagatc ccagagttag gggcctatat 420
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 tga 1203

<210> 46
 <211> 400
 <212> PRT
 <213> Hepatitis B virus

<400> 46

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
 305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
 325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
 340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
 355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
 370 375 380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 385 390 395 400

<210> 47
 <211> 799
 <212> DNA
 <213> Homo sapiens

<400> 47
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 cccaaccatt cccttatcca ggccttttga caacgctatg ctccgcgccc atcgtctgca 180
 ccagctggcc tttagacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa 240
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ggtgtacggc gcctctgaca gcaacgtcta tgacctccta aaggacctag aggaaggcat 480
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gacctacagc aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg 600
gctgctctac tgcttcagga aggacatgga caaggctgag acattcctgc gcacgtgca 660
gtgccgtctt gtggagggca gctgtggctt ctagctgccc ggggtggcatc cctgtgaccc 720
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<210> 48
<211> 217
<212> PRT
<213> Homo sapiens

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```

<400> 48

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```

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1           5           10           15

```

```

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
          20           25           30

```

```

Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
          35           40           45

```

```

Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
          50           55           60

```

```

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65           70           75           80

```

```

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
          85           90           95

```

```

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
          100          105          110

```

```

Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
          115          120          125

```


Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
 130 135 140

Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
 145 150 155 160

Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
 165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
 180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
 195 200 205

Arg Ser Val Glu Gly Ser Cys Gly Phe
 210 215

<210> 49
 <211> 963
 <212> DNA
 <213> Homo sapiens

<400> 49
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 gtcccgcccg agtgcttcga cctgctggtc cggcactgct tggcctgcgg gctcctgcgc 180
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 caggagtcgg tgggcgcggg ggccggcgag gcggcggtcg acaaaactca cacatgccca 300
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 aaggacaccc tcatgatctc ccggaccctt gaggtcacat gcgtgggtgt ggacgtgagc 420
 cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 480
 aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtgggtcag cgtcctcacc 540
 gtccctgcacc aggactgggt gaatggcaag gactacaagt gcaaggtctc caacaaagcc 600
 ctccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 660
 gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgaacctgc 720
 ctgggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 780

gagaacaact acaagaccac gcctcccggtg ttggactccg acggctcctt cttcctctac 840
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 tga 963

<210> 50
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 50

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg
 20 25 30

Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
 35 40 45

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
 50 55 60

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
 65 70 75 80

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
 85 90 95

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 100 105 110

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 115 120 125

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 130 135 140

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 145 150 155 160

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
 100 105

<210> 52
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 52

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 53
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 53

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 54

<211> 119

<212> PRT

<213> Mus musculus

<400> 54

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr
 1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly
 100 105 110

Thr Leu Val Thr Val Ser Ala
 115

<210> 55
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 55

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 56
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 56

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr

340

345

350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

<210> 57
 <211> 8540
 <212> DNA
 <213> Homo sapiens

<400> 57
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 ggagaatggg cgggaactggg cggagttagg ggcgggatgg gcggagttag gggcgggact 180
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 gactttccac acctgggttg tgactaattg agatgcatgc tttgcatact tctgctgct 300
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 gttacataac ttacggtaaa tggcccgctt ggctgaccgc ccaacgaccc ccgcccattg 480
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atgggtgatgc ggttttggca gtacatcaat gggcgtggat agcggtttga ctcacgggga	780
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ctcccagggtg cacgatgtga tggtagcaag gtggaaatca aacgtacggg ggctgcacca	1080
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttctg	1140
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